

SEQUENCE LISTING

<110> E. I. duPont de Nemours and Company, Inc.
Suh, Wonchul
Rouviere, Pierre
Cheng, Qiong

<120> Increasing Carotenoid Production in Bacteria Via Chromosomal
Integration

<130> CL2027 US NA

<150> US 60/434618
<151> 2002-12-19

<160> 66

<170> PatentIn version 3.2

<210> 1
<211> 912
<212> DNA
<213> Pantoea stewartii

<220>
<221> misc_feature
<222> (1)..(3)
<223> ttg alternative start codon used to encode methionine

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gggtgccgca tgcgtgaagg cacgctggca ccgggcaaac gtattcgtcc gatgctgctg 180
ttattaacag cgcgcatct tggctgtgcg atcagtcacg ggggattact ggatttagcc 240
tgcgcggttg aaatggtgca tgctgcctcg ctgattctgg atgatatgcc ctgcatggac 300
gatgcgcaga tgcgtcgggg gcgtcccacc attcacacgc agtacggtga acatgtggcg 360
attctggcgg cggctcgttt actcagcaaa gcgtttgggg tgattgccga ggctgaagggt 420
ctgacgccga tagccaaaac tcgcgcggtg tcggagctgt ccactgcatg tggcatgcag 480
gggtctggttc agggccagtt taaggacctc tcggaaggcg ataaaccccg cagcgccgat 540
gccatactgc taaccaatca gtttaaaacc agcacgctgt tttgcgcgtc aacgcaaattg 600
gcgtccattg cggccaacgc gtcctgcgaa gcgcgtgaga acctgcatcg tttctcgctc 660
gatctcggcc aggcctttca gttgcttgac gatcttaccg atggcatgac cgataccggc 720
aaagacatca atcaggatgc aggtaaatca acgctggtca atttattagg ctcaggcgcg 780
gtcgaagaac gcctgcgaca gcatttgcgct ctggccagtg aacacctttc cgcggcgatgc 840
caaaacggcc attccaccac ccaacttttt attcaggcct ggtttgacaa aaaactcgct 900
gccgtcagtt aa 912

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<212> PRT
<213> Pantoea stewartii

<400> 2

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20 25 30
Val Gln Gly Glu Arg Asp Cys Val Gly Ala Ala Met Arg Glu Gly Thr
35 40 45
Leu Ala Pro Gly Lys Arg Ile Arg Pro Met Leu Leu Leu Thr Ala
50 55 60
Arg Asp Leu Gly Cys Ala Ile Ser His Gly Gly Leu Leu Asp Leu Ala
65 70 75 80
Cys Ala Val Glu Met Val His Ala Ala Ser Leu Ile Leu Asp Asp Met
85 90 95
Pro Cys Met Asp Asp Ala Gln Met Arg Arg Gly Arg Pro Thr Ile His
100 105 110
Thr Gln Tyr Gly Glu His Val Ala Ile Leu Ala Ala Val Ala Leu Leu
115 120 125
Ser Lys Ala Phe Gly Val Ile Ala Glu Ala Glu Gly Leu Thr Pro Ile
130 135 140
Ala Lys Thr Arg Ala Val Ser Glu Leu Ser Thr Ala Ile Gly Met Gln
145 150 155 160
Gly Leu Val Gln Gly Gln Phe Lys Asp Leu Ser Glu Gly Asp Lys Pro
165 170 175
Arg Ser Ala Asp Ala Ile Leu Leu Thr Asn Gln Phe Lys Thr Ser Thr
180 185 190
Leu Phe Cys Ala Ser Thr Gln Met Ala Ser Ile Ala Ala Asn Ala Ser
195 200 205
Cys Glu Ala Arg Glu Asn Leu His Arg Phe Ser Leu Asp Leu Gly Gln
210 215 220
Ala Phe Gln Leu Leu Asp Asp Leu Thr Asp Gly Met Thr Asp Thr Gly
225 230 235 240
Lys Asp Ile Asn Gln Asp Ala Gly Lys Ser Thr Leu Val Asn Leu Leu
245 250 255
Gly Ser Gly Ala Val Glu Glu Arg Leu Arg Gln His Leu Arg Leu Ala
260 265 270

Ser Glu His Leu Ser Ala Ala Cys Gln Asn Gly His Ser Thr Thr Gln
 275 280 285

Leu Phe Ile Gln Ala Trp Phe Asp Lys Lys Leu Ala Ala Val Ser
 290 295 300

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 gct ctg caa aac ctt gct cag gaa tta gtg gcc cgc ggt cat cgt gtt 96
 Ala Leu Gln Asn Leu Ala Gln Glu Leu Val Ala Arg Gly His Arg Val
 20 25 30
 acg ttt ttt cag caa cat gac tgc aaa gcg ctg gta acg ggc agc gat 144
 Thr Phe Phe Gln Gln His Asp Cys Lys Ala Leu Val Thr Gly Ser Asp
 35 40 45
 atc gga ttc cag acc gtc gga ctg caa acg cat cct ccc ggt tcc tta 192
 Ile Gly Phe Gln Thr Val Gly Leu Gln Thr His Pro Pro Gly Ser Leu
 50 55 60
 tcg cac ctg ctg cac ctg gcc gcg cac cca ctc gga ccc tcg atg tta 240
 Ser His Leu Leu His Leu Ala Ala His Pro Leu Gly Pro Ser Met Leu
 65 70 75
 cga ctg atc aat gaa atg gca cgt acc agc gat atg ctt tgc cgg gaa 288
 Arg Leu Ile Asn Glu Met Ala Arg Thr Ser Asp Met Leu Cys Arg Glu
 85 90 95
 ctg ccc gcc gct ttt cat gcg ttg cag ata gag ggc gtg atc gtt gat 336
 Leu Pro Ala Ala Phe His Ala Leu Gln Ile Glu Gly Val Ile Val Asp
 100 105 110
 caa atg gag ccg gca ggt gca gta gtc gca gaa gcg tca ggt ctg ccg 384
 Gln Met Glu Pro Ala Gly Ala Val Val Ala Glu Ala Ser Gly Leu Pro
 115 120 125
 ttt gtt tcg gtg gcc tgc gcg ctg ccg ctc aac cgc gaa ccg ggt ttg 432
 Phe Val Ser Val Ala Cys Ala Leu Pro Leu Asn Arg Glu Pro Gly Leu
 130 135 140
 cct ctg gcg gtg atg cct ttc gag tac ggc acc agc gat gcg gct cgg 480
 Pro Leu Ala Val Met Pro Phe Glu Tyr Gly Thr Ser Asp Ala Ala Arg
 145 150 155 160
 gaa cgc tat acc acc agc gaa aaa att tat gac tgg ctg atg cga cgt 528
 Glu Arg Tyr Thr Thr Ser Glu Lys Ile Tyr Asp Trp Leu Met Arg Arg
 165 170 175
 cac gat cgt gtg atc gcg cat cat gca tgc aga atg ggt tta gcc ccg 576
 His Asp Arg Val Ile Ala His His Ala Cys Arg Met Gly Leu Ala Pro
 180 185 190
 cgt gaa aaa ctg cat cat tgt ttt tct cca ctg gca caa atc agc cag 624

Arg	Glu	Lys	Leu	His	His	Cys	Phe	Ser	Pro	Leu	Ala	Gln	Ile	Ser	Gln	
		195					200					205				
ttg	atc	ccc	gaa	ctg	gat	ttt	ccc	cgc	aaa	gcg	ctg	cca	gac	tgc	ttt	672
Leu	Ile	Pro	Glu	Leu	Asp	Phe	Pro	Arg	Lys	Ala	Leu	Pro	Asp	Cys	Phe	
	210					215					220					
cat	gcg	gtt	gga	ccg	tta	cgg	caa	ccc	cag	ggg	acg	ccg	ggg	tca	tca	720
His	Ala	Val	Gly	Pro	Leu	Arg	Gln	Pro	Gln	Gly	Thr	Pro	Gly	Ser	Ser	
	225				230					235					240	
act	tct	tat	ttt	ccg	tcc	ccg	gac	aaa	ccc	cgt	att	ttt	gcc	tcg	ctg	768
Thr	Ser	Tyr	Phe	Pro	Ser	Pro	Asp	Lys	Pro	Arg	Ile	Phe	Ala	Ser	Leu	
				245					250					255		
ggc	acc	ctg	cag	gga	cat	cgt	tat	ggc	ctg	ttc	agg	acc	atc	gcc	aaa	816
Gly	Thr	Leu	Gln	Gly	His	Arg	Tyr	Gly	Leu	Phe	Arg	Thr	Ile	Ala	Lys	
			260					265					270			
gcc	tgc	gaa	gag	gtg	gat	gcg	cag	tta	ctg	ttg	gca	cac	tgt	ggc	ggc	864
Ala	Cys	Glu	Glu	Val	Asp	Ala	Gln	Leu	Leu	Leu	Ala	His	Cys	Gly	Gly	
		275					280					285				
ctc	tca	gcc	acg	cag	gca	ggt	gaa	ctg	gcc	cgg	ggc	ggg	gac	att	cag	912
Leu	Ser	Ala	Thr	Gln	Ala	Gly	Glu	Leu	Ala	Arg	Gly	Gly	Asp	Ile	Gln	
	290					295					300					
gtt	gtg	gat	ttt	gcc	gat	caa	tcc	gca	gca	ctt	tca	cag	gca	cag	ttg	960
Val	Val	Asp	Phe	Ala	Asp	Gln	Ser	Ala	Ala	Leu	Ser	Gln	Ala	Gln	Leu	
	305				310					315					320	
aca	atc	aca	cat	ggt	ggg	atg	aat	acg	gta	ctg	gac	gct	att	gct	tcc	1008
Thr	Ile	Thr	His	Gly	Gly	Met	Asn	Thr	Val	Leu	Asp	Ala	Ile	Ala	Ser	
				325					330					335		
cgc	aca	ccg	cta	ctg	gcg	ctg	ccg	ctg	gca	ttt	gat	caa	cct	ggc	gtg	1056
Arg	Thr	Pro	Leu	Leu	Ala	Leu	Pro	Leu	Ala	Phe	Asp	Gln	Pro	Gly	Val	
			340				345						350			
gca	tca	cga	att	gtt	tat	cat	ggc	atc	ggc	aag	cgt	gcg	tct	cgg	ttt	1104
Ala	Ser	Arg	Ile	Val	Tyr	His	Gly	Ile	Gly	Lys	Arg	Ala	Ser	Arg	Phe	
		355					360					365				
act	acc	agc	cat	gcg	ctg	gcg	cgg	cag	att	cga	tcg	ctg	ctg	act	aac	1152
Thr	Thr	Ser	His	Ala	Leu	Ala	Arg	Gln	Ile	Arg	Ser	Leu	Leu	Thr	Asn	
	370					375					380					
acc	gat	tac	ccg	cag	cgt	atg	aca	aaa	att	cag	gcc	gca	ttg	cgt	ctg	1200
Thr	Asp	Tyr	Pro	Gln	Arg	Met	Thr	Lys	Ile	Gln	Ala	Ala	Leu	Arg	Leu	
	385				390					395					400	
gca	ggc	ggc	aca	cca	gcc	gcc	gcc	gat	att	gtt	gaa	cag	gcg	atg	cgg	1248
Ala	Gly	Gly	Thr	Pro	Ala	Ala	Ala	Asp	Ile	Val	Glu	Gln	Ala	Met	Arg	
				405					410					415		
acc	tgt	cag	cca	gta	ctc	agt	ggg	cag	gat	tat	gca	acc	gca	cta	tga	1296
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 <213> Pantoea stewartii

<400> 4

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 20 25 30
 Thr Phe Phe Gln Gln His Asp Cys Lys Ala Leu Val Thr Gly Ser Asp
 35 40 45
 Ile Gly Phe Gln Thr Val Gly Leu Gln Thr His Pro Pro Gly Ser Leu
 50 55 60
 Ser His Leu Leu His Leu Ala Ala His Pro Leu Gly Pro Ser Met Leu
 65 70 75 80
 Arg Leu Ile Asn Glu Met Ala Arg Thr Ser Asp Met Leu Cys Arg Glu
 85 90 95
 Leu Pro Ala Ala Phe His Ala Leu Gln Ile Glu Gly Val Ile Val Asp
 100 105 110
 Gln Met Glu Pro Ala Gly Ala Val Val Ala Glu Ala Ser Gly Leu Pro
 115 120 125
 Phe Val Ser Val Ala Cys Ala Leu Pro Leu Asn Arg Glu Pro Gly Leu
 130 135 140
 Pro Leu Ala Val Met Pro Phe Glu Tyr Gly Thr Ser Asp Ala Ala Arg
 145 150 155 160
 Glu Arg Tyr Thr Thr Ser Glu Lys Ile Tyr Asp Trp Leu Met Arg Arg
 165 170 175
 His Asp Arg Val Ile Ala His His Ala Cys Arg Met Gly Leu Ala Pro
 180 185 190
 Arg Glu Lys Leu His His Cys Phe Ser Pro Leu Ala Gln Ile Ser Gln
 195 200 205
 Leu Ile Pro Glu Leu Asp Phe Pro Arg Lys Ala Leu Pro Asp Cys Phe
 210 215 220
 His Ala Val Gly Pro Leu Arg Gln Pro Gln Gly Thr Pro Gly Ser Ser
 225 230 235 240
 Thr Ser Tyr Phe Pro Ser Pro Asp Lys Pro Arg Ile Phe Ala Ser Leu
 245 250 255
 Gly Thr Leu Gln Gly His Arg Tyr Gly Leu Phe Arg Thr Ile Ala Lys
 260 265 270
 Ala Cys Glu Glu Val Asp Ala Gln Leu Leu Leu Ala His Cys Gly Gly
 275 280 285

Leu Ser Ala Thr Gln Ala Gly Glu Leu Ala Arg Gly Gly Asp Ile Gln
 290 295 300
 Val Val Asp Phe Ala Asp Gln Ser Ala Ala Leu Ser Gln Ala Gln Leu
 305 310 315 320
 Thr Ile Thr His Gly Gly Met Asn Thr Val Leu Asp Ala Ile Ala Ser
 325 330 335
 Arg Thr Pro Leu Leu Ala Leu Pro Leu Ala Phe Asp Gln Pro Gly Val
 340 345 350
 Ala Ser Arg Ile Val Tyr His Gly Ile Gly Lys Arg Ala Ser Arg Phe
 355 360 365
 Thr Thr Ser His Ala Leu Ala Arg Gln Ile Arg Ser Leu Leu Thr Asn
 370 375 380
 Thr Asp Tyr Pro Gln Arg Met Thr Lys Ile Gln Ala Ala Leu Arg Leu
 385 390 395 400
 Ala Gly Gly Thr Pro Ala Ala Ala Asp Ile Val Glu Gln Ala Met Arg
 405 410 415
 Thr Cys Gln Pro Val Leu Ser Gly Gln Asp Tyr Ala Thr Ala Leu
 420 425 430

<210> 5
 <211> 1149
 <212> DNA
 <213> Pantoea stewartii

<220>
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ggc ctt atc gcg ctc cgg ctt cag caa cag cat ccg gat atg cgg atc	96
Gly Leu Ile Ala Leu Arg Leu Gln Gln His Pro Asp Met Arg Ile	
20 25 30	
ttg ctt att gag gcg ggt cct gag gcg gga ggg aac cat acc tgg tcc	144
Leu Leu Ile Glu Ala Gly Pro Glu Ala Gly Gly Asn His Thr Trp Ser	
35 40 45	
ttt cac gaa gag gat tta acg ctg aat cag cat cgc tgg ata gcg ccg	192
Phe His Glu Glu Asp Leu Thr Leu Asn Gln His Arg Trp Ile Ala Pro	
50 55 60	
ctt gtg gtc cat cac tgg ccc gac tac cag gtt cgt ttc ccc caa cgc	240
Leu Val Val His His Trp Pro Asp Tyr Gln Val Arg Phe Pro Gln Arg	
65 70 75 80	
cgt cgc cat gtg aac agt ggc tac tac tgc gtg acc tcc cgg cat ttc	288

Arg	Arg	His	Val	Asn 85	Ser	Gly	Tyr	Tyr	Cys 90	Val	Thr	Ser	Arg	His 95	Phe	
gcc Ala	ggg Gly	ata Ile	ctc Leu 100	cgg Arg	caa Gln	cag Gln	ttt Phe	gga Gly 105	caa Gln	cat His	tta Leu	tgg Trp	ctg Leu 110	cat His	acc Thr	336
gcg Ala	gtt Val	tca Ser 115	gcc Ala	gtt Val	cat His	gct Ala	gaa Glu 120	tcg Ser	gtc Val	cag Gln	tta Leu	gcg Ala 125	gat Asp	ggc Gly	cgg Arg	384
att Ile	att Ile 130	cat His	gcc Ala	agt Ser	aca Thr	gtg Val 135	atc Ile	gac Asp	gga Gly	cgg Arg	ggt Gly 140	tac Tyr	acg Thr	cct Pro	gat Asp	432
tct Ser 145	gca Ala	cta Leu	cgc Arg	gta Val	gga Gly 150	ttc Phe	cag Gln	gca Ala	ttt Phe 155	atc Ile	ggt Gly	cag Gln	gag Glu	tgg Trp	caa Gln 160	480
ctg Leu	agc Ser	gcg Ala	ccg Pro	cat His 165	ggt Gly	tta Leu	tcg Ser	tca Ser	ccg Pro 170	att Ile	atc Ile	atg Met	gat Asp	gcg Ala 175	acg Thr	528
gtc Val	gat Asp	cag Gln	caa Gln 180	aat Asn	ggc Gly	tac Tyr	cgc Arg	ttt Phe 185	gtt Val	tat Tyr	acc Thr	ctg Leu	ccg Pro 190	ctt Leu	tcc Ser	576
gca Ala	acc Thr	gca Ala 195	ctg Leu	ctg Leu	atc Ile	gaa Glu	gac Asp 200	aca Thr	cac His	tac Tyr	att Ile	gac Asp 205	aag Lys	gct Ala	aat Asn	624
ctt Leu	cag Gln 210	gcc Ala	gaa Glu	cgg Arg	gcg Ala	cgt Arg 215	cag Gln	aac Asn	att Ile	cgc Arg	gat Asp 220	tat Tyr	gct Ala	gcg Ala	cga Arg	672
cag Gln 225	ggt Gly	tgg Trp	ccg Pro	tta Leu	cag Gln 230	acg Thr	ttg Leu	ctg Leu	cgg Arg	gaa Glu 235	gaa Glu	cag Gln	ggt Gly	gca Ala	ttg Leu 240	720
ccc Pro	att Ile	acg Thr	tta Leu	acg Thr 245	ggc Gly	gat Asp	aat Asn	cgt Arg	cag Gln 250	ttt Phe	tgg Trp	caa Gln	cag Gln	caa Gln 255	ccg Pro	768
caa Gln	gcc Ala	tgt Cys	agc Ser 260	gga Gly	tta Leu	cgc Arg	gcc Ala	ggg Gly 265	ctg Leu	ttt Phe	cat His	ccg Pro	aca Thr 270	acc Thr	ggc Gly	816
tac Tyr	tcc Ser	cta Leu 275	ccg Pro	ctc Leu	gcg Ala	gtg Val	gcg Ala 280	ctg Leu	gcc Ala	gat Asp	cgt Arg	ctc Leu 285	agc Ser	gcg Ala	ctg Leu	864
gat Asp	gtg Val 290	ttt Phe	acc Thr	tct Ser	tcc Ser	tct Ser 295	gtt Val	cac His	cag Gln	acg Thr	att Ile 300	gct Ala	cac His	ttt Phe	gcc Ala	912
cag Gln 305	caa Gln	cgt Arg	tgg Trp	cag Gln	caa Gln 310	cag Gln	ggg Gly	ttt Phe	ttc Phe 315	cgc Arg	atg Met	ctg Leu	aat Asn	cgc Arg	atg Met 320	960
ttg Leu	ttt Phe	tta Leu	gcc Ala	gga Gly 325	ccg Pro	gcc Ala	gag Glu	tca Ser	cgc Arg 330	tgg Trp	cgt Arg	gtg Val	atg Met	cag Gln 335	cgt Arg	1008
ttc Phe	tat Tyr	ggc Gly	tta Leu 340	ccc Pro	gag Glu	gat Asp	ttg Leu	att Ile 345	gcc Ala	cgc Arg	ttt Phe	tat Tyr	gcg Ala 350	gga Gly	aaa Lys	1056
ctc Leu	acc Thr	gtg Val	acc Thr	gat Asp	cgg Arg	cta Leu	cgc Arg	att Ile	ctg Leu	agc Ser	ggc Gly	aag Lys	ccg Pro	ccc Pro	gtt Val	1104

355	360	365	
ccc gtt ttc gcg gca ttg cag gca att atg acg act cat cgt tga			1149
Pro Val Phe Ala Ala Leu Gln Ala Ile Met Thr Thr His Arg			
370	375	380	

<210> 6
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 <212> PRT
 <213> Pantoea stewartii

<400> 6

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Gly Leu Ile Ala Leu Arg Leu Gln Gln Gln His Pro Asp Met Arg Ile
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Leu Leu Ile Glu Ala Gly Pro Glu Ala Gly Gly Asn His Thr Trp Ser
35 40 45

Phe His Glu Glu Asp Leu Thr Leu Asn Gln His Arg Trp Ile Ala Pro
50 55 60

Leu Val Val His His Trp Pro Asp Tyr Gln Val Arg Phe Pro Gln Arg
65 70 75 80

Arg Arg His Val Asn Ser Gly Tyr Tyr Cys Val Thr Ser Arg His Phe
85 90 95

Ala Gly Ile Leu Arg Gln Gln Phe Gly Gln His Leu Trp Leu His Thr
100 105 110

Ala Val Ser Ala Val His Ala Glu Ser Val Gln Leu Ala Asp Gly Arg
115 120 125

Ile Ile His Ala Ser Thr Val Ile Asp Gly Arg Gly Tyr Thr Pro Asp
130 135 140

Ser Ala Leu Arg Val Gly Phe Gln Ala Phe Ile Gly Gln Glu Trp Gln
145 150 155 160

Leu Ser Ala Pro His Gly Leu Ser Ser Pro Ile Ile Met Asp Ala Thr
165 170 175

Val Asp Gln Gln Asn Gly Tyr Arg Phe Val Tyr Thr Leu Pro Leu Ser
180 185 190

Ala Thr Ala Leu Leu Ile Glu Asp Thr His Tyr Ile Asp Lys Ala Asn
195 200 205

Leu Gln Ala Glu Arg Ala Arg Gln Asn Ile Arg Asp Tyr Ala Ala Arg
210 215 220

Gln Gly Trp Pro Leu Gln Thr Leu Leu Arg Glu Glu Gln Gly Ala Leu
 225 230 235 240
 Pro Ile Thr Leu Thr Gly Asp Asn Arg Gln Phe Trp Gln Gln Gln Pro
 245 250 255
 Gln Ala Cys Ser Gly Leu Arg Ala Gly Leu Phe His Pro Thr Thr Gly
 260 265 270
 Tyr Ser Leu Pro Leu Ala Val Ala Leu Ala Asp Arg Leu Ser Ala Leu
 275 280 285
 Asp Val Phe Thr Ser Ser Ser Val His Gln Thr Ile Ala His Phe Ala
 290 295 300
 Gln Gln Arg Trp Gln Gln Gln Gly Phe Phe Arg Met Leu Asn Arg Met
 305 310 315 320
 Leu Phe Leu Ala Gly Pro Ala Glu Ser Arg Trp Arg Val Met Gln Arg
 325 330 335
 Phe Tyr Gly Leu Pro Glu Asp Leu Ile Ala Arg Phe Tyr Ala Gly Lys
 340 345 350
 Leu Thr Val Thr Asp Arg Leu Arg Ile Leu Ser Gly Lys Pro Pro Val
 355 360 365
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 370 375 380

<210> 7
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 <212> DNA
 <213> *Pantoea stewartii*

<220>
 <221> CDS
 <222> (1)..(1479)

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gca att cgt tta cag gcc gca ggt att cct gtt ttg ctg ctt gag cag	96
Ala Ile Arg Leu Gln Ala Ala Gly Ile Pro Val Leu Leu Leu Glu Gln	
20 25 30	
cgc gac aag ccg ggt ggc cgg gct tat gtt tat cag gag cag ggc ttt	144
Arg Asp Lys Pro Gly Gly Arg Ala Tyr Val Tyr Gln Glu Gln Gly Phe	
35 40 45	
act ttt gat gca ggc cct acc gtt atc acc gat ccc agc gcg att gaa	192
Thr Phe Asp Ala Gly Pro Thr Val Ile Thr Asp Pro Ser Ala Ile Glu	
50 55 60	
gaa ctg ttt gct ctg gcc ggt aaa cag ctt aag gat tac gtc gag ctg	240

Glu 65	Leu	Phe	Ala	Leu	Ala 70	Gly	Lys	Gln	Leu	Lys 75	Asp	Tyr	Val	Glu	Leu 80	
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ttc Phe	aat Asn	tac Tyr	gat Asp 100	aac Asn	gac Asp	cag Gln	gcc Ala	cag Gln 105	tta Leu	gaa Glu	gcg Ala	cag Gln 110	ata Ile	cag Gln	cag Gln	336
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cgt Arg	gcc Ala 130	gta Val	ttc Phe	aat Asn	gag Glu	ggc Gly 135	tat Tyr	ctg Leu	aag Lys	ctc Leu	ggc Gly 140	act Thr	gtg Val	cct Pro	ttt Phe	432
tta Leu 145	tcg Ser	ttc Phe	aaa Lys	gac Asp	atg Met 150	ctt Leu	cgg Arg	gcc Ala	gcg Ala	ccc Pro 155	cag Gln	ttg Leu	gca Ala	aag Lys	ctg Leu 160	480
cag Gln	gca Ala	tgg Trp	cgc Arg	agc Ser 165	gtt Val	tac Tyr	agt Ser	aaa Lys	gtt Val 170	gcc Ala	ggc Gly	tac Tyr	att Ile	gag Glu 175	gat Asp	528
gag Glu	cat His	ctt Leu	cgg Arg 180	cag Gln	gcg Ala	ttt Phe	tct Ser	ttt Phe 185	cac His	tcg Ser	ctc Leu	tta Leu	gtg Val 190	ggg Gly	ggg Gly	576
aat Asn	ccg Pro	ttt Phe 195	gca Ala	acc Thr	tcg Ser	tcc Ser	att Ile 200	tat Tyr	acg Thr	ctg Leu	att Ile	cac His 205	gcg Ala	tta Leu	gaa Glu	624
cgg Arg	gaa Glu 210	tgg Trp	ggc Gly	gtc Val	tgg Trp	ttt Phe 215	cca Pro	cgc Arg	ggt Gly	gga Gly	acc Thr 220	ggt Gly	gcg Ala	ctg Leu	gtc Val	672
aat Asn 225	ggc Gly	atg Met	atc Ile	aag Lys	ctg Leu 230	ttt Phe	cag Gln	gat Asp	ctg Leu	ggc Gly 235	ggc Gly	gaa Glu	gtc Val	gtg Val	ctt Leu 240	720
aac Asn	gcc Ala	cgg Arg	gtc Val	agt Ser 245	cat His	atg Met	gaa Glu	acc Thr	gtt Val 250	ggg Gly	gac Asp	aag Lys	att Ile	cag Gln 255	gcc Ala	768
gtg Val	cag Gln	ttg Leu	gaa Glu 260	gac Asp	ggc Gly	aga Arg	cgg Arg	ttt Phe 265	gaa Glu	acc Thr	tgc Cys	gcg Ala	gtg Val 270	gcg Ala	tcg Ser	816
aac Asn	gct Ala	gat Asp 275	gtt Val	gta Val	cat His	acc Thr	tat Tyr 280	cgc Arg	gat Asp	ctg Leu	ctg Leu	tct Ser 285	cag Gln	cat His	ccc Pro	864
gca Ala	gcc Ala 290	gct Ala	aag Lys	cag Gln	gcg Ala	aaa Lys 295	aaa Lys	ctg Leu	caa Gln	tcc Ser	aag Lys 300	cgt Arg	atg Met	agt Ser	aac Asn	912
tca Ser 305	ctg Leu	ttt Phe	gta Val	ctc Leu	tat Tyr 310	ttt Phe	ggt Gly	ctc Leu	aac Asn	cat His 315	cat His	cac His	gat Asp	caa Gln	ctc Leu 320	960
gcc Ala	cat His	cat His	acc Thr	gtc Val 325	tgt Cys	ttt Phe	ggg Gly	cca Pro	cgc Arg 330	tac Tyr	cgt Arg	gaa Glu	ctg Leu	att Ile 335	cac His	1008
gaa Glu	att Ile	ttt Phe	aac Asn	cat His	gat Asp	ggt Gly	ctg Leu	gct Ala	gag Glu	gat Asp	ttt Phe	tcg Ser	ctt Leu	tat Tyr	tta Leu	1056

340										345					350					
cac	gca	cct	tgt	gtc	acg	gat	ccg	tca	ctg	gca	ccg	gaa	ggg	tgc	ggc	1104				
His	Ala	Pro	Cys	Val	Thr	Asp	Pro	Ser	Leu	Ala	Pro	Glu	Gly	Cys	Gly					
		355					360					365								
agc	tat	tat	gtg	ctg	gcg	cct	gtt	cca	cac	tta	ggc	acg	gcg	aac	ctc	1152				
Ser	Tyr	Tyr	Val	Leu	Ala	Pro	Val	Pro	His	Leu	Gly	Thr	Ala	Asn	Leu					
	370					375					380									
gac	tgg	gcg	gta	gaa	gga	ccc	cga	ctg	cgc	gat	cgt	att	ttt	gac	tac	1200				
Asp	Trp	Ala	Val	Glu	Gly	Pro	Arg	Leu	Arg	Asp	Arg	Ile	Phe	Asp	Tyr					
				390						395					400					
ctt	gag	caa	cat	tac	atg	cct	ggc	ttg	cga	agc	cag	ttg	gtg	acg	cac	1248				
Leu	Glu	Gln	His	Tyr	Met	Pro	Gly	Leu	Arg	Ser	Gln	Leu	Val	Thr	His					
				405					410					415						
cgt	atg	ttt	acg	ccg	ttc	gat	ttc	cgc	gac	gag	ctc	aat	gcc	tgg	caa	1296				
Arg	Met	Phe	Thr	Pro	Phe	Asp	Phe	Arg	Asp	Glu	Leu	Asn	Ala	Trp	Gln					
			420					425					430							
ggt	tcg	gcc	ttc	tcg	gtt	gaa	cct	att	ctg	acc	cag	agc	gcc	tgg	ttc	1344				
Gly	Ser	Ala	Phe	Ser	Val	Glu	Pro	Ile	Leu	Thr	Gln	Ser	Ala	Trp	Phe					
		435					440					445								
cga	cca	cat	aac	cgc	gat	aag	cac	att	gat	aat	ctt	tat	ctg	gtt	ggc	1392				
Arg	Pro	His	Asn	Arg	Asp	Lys	His	Ile	Asp	Asn	Leu	Tyr	Leu	Val	Gly					
	450					455					460									
gca	ggc	acc	cat	cct	ggc	gcg	ggc	att	ccc	ggc	gta	atc	ggc	tcg	gcg	1440				
Ala	Gly	Thr	His	Pro	Gly	Ala	Gly	Ile	Pro	Gly	Val	Ile	Gly	Ser	Ala					
	465				470					475					480					
aag	gcg	acg	gca	ggc	tta	atg	ctg	gag	gac	ctg	att	tga				1479				
Lys	Ala	Thr	Ala	Gly	Leu	Met	Leu	Glu	Asp	Leu	Ile									
				485					490											

<210> 8
 <211> 492
 <212> PRT
 <213> Pantoea stewartii
 <400> 8

Met	Lys	Pro	Thr	Thr	Val	Ile	Gly	Ala	Gly	Phe	Gly	Gly	Leu	Ala	Leu
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Ala	Ile	Arg	Leu	Gln	Ala	Ala	Gly	Ile	Pro	Val	Leu	Leu	Leu	Glu	Gln
			20				25						30		
Arg	Asp	Lys	Pro	Gly	Gly	Arg	Ala	Tyr	Val	Tyr	Gln	Glu	Gln	Gly	Phe
		35					40					45			
Thr	Phe	Asp	Ala	Gly	Pro	Thr	Val	Ile	Thr	Asp	Pro	Ser	Ala	Ile	Glu
	50					55				60					
Glu	Leu	Phe	Ala	Leu	Ala	Gly	Lys	Gln	Leu	Lys	Asp	Tyr	Val	Glu	Leu
65					70					75					80
Leu	Pro	Val	Thr	Pro	Phe	Tyr	Arg	Leu	Cys	Trp	Glu	Ser	Gly	Lys	Val
				85					90					95	

Phe Asn Tyr Asp Asn Asp Gln Ala Gln Leu Glu Ala Gln Ile Gln Gln
100 105 110
Phe Asn Pro Arg Asp Val Ala Gly Tyr Arg Ala Phe Leu Asp Tyr Ser
115 120 125
Arg Ala Val Phe Asn Glu Gly Tyr Leu Lys Leu Gly Thr Val Pro Phe
130 135 140
Leu Ser Phe Lys Asp Met Leu Arg Ala Ala Pro Gln Leu Ala Lys Leu
145 150 155 160
Gln Ala Trp Arg Ser Val Tyr Ser Lys Val Ala Gly Tyr Ile Glu Asp
165 170 175
Glu His Leu Arg Gln Ala Phe Ser Phe His Ser Leu Leu Val Gly Gly
180 185 190
Asn Pro Phe Ala Thr Ser Ser Ile Tyr Thr Leu Ile His Ala Leu Glu
195 200 205
Arg Glu Trp Gly Val Trp Phe Pro Arg Gly Gly Thr Gly Ala Leu Val
210 215 220
Asn Gly Met Ile Lys Leu Phe Gln Asp Leu Gly Gly Glu Val Val Leu
225 230 235 240
Asn Ala Arg Val Ser His Met Glu Thr Val Gly Asp Lys Ile Gln Ala
245 250 255
Val Gln Leu Glu Asp Gly Arg Arg Phe Glu Thr Cys Ala Val Ala Ser
260 265 270
Asn Ala Asp Val Val His Thr Tyr Arg Asp Leu Leu Ser Gln His Pro
275 280 285
Ala Ala Ala Lys Gln Ala Lys Lys Leu Gln Ser Lys Arg Met Ser Asn
290 295 300
Ser Leu Phe Val Leu Tyr Phe Gly Leu Asn His His His Asp Gln Leu
305 310 315 320
Ala His His Thr Val Cys Phe Gly Pro Arg Tyr Arg Glu Leu Ile His
325 330 335
Glu Ile Phe Asn His Asp Gly Leu Ala Glu Asp Phe Ser Leu Tyr Leu
340 345 350
His Ala Pro Cys Val Thr Asp Pro Ser Leu Ala Pro Glu Gly Cys Gly
355 360 365

Ser Tyr Tyr Val Leu Ala Pro Val Pro His Leu Gly Thr Ala Asn Leu
 370 375 380
 Asp Trp Ala Val Glu Gly Pro Arg Leu Arg Asp Arg Ile Phe Asp Tyr
 385 390 395 400
 Leu Glu Gln His Tyr Met Pro Gly Leu Arg Ser Gln Leu Val Thr His
 405 410 415
 Arg Met Phe Thr Pro Phe Asp Phe Arg Asp Glu Leu Asn Ala Trp Gln
 420 425 430
 Gly Ser Ala Phe Ser Val Glu Pro Ile Leu Thr Gln Ser Ala Trp Phe
 435 440 445
 Arg Pro His Asn Arg Asp Lys His Ile Asp Asn Leu Tyr Leu Val Gly
 450 455 460
 Ala Gly Thr His Pro Gly Ala Gly Ile Pro Gly Val Ile Gly Ser Ala
 465 470 475 480
 Lys Ala Thr Ala Gly Leu Met Leu Glu Asp Leu Ile
 485 490

<210> 9
 <211> 891
 <212> DNA
 <213> *Pantoea stewartii*

<220>
 <221> CDS
 <222> (1)..(891)

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gcc aaa acc cgt cgc agc gtg ctg atg ctt tac gca tgg tgc cgc cac	96
Ala Lys Thr Arg Arg Ser Val Leu Met Leu Tyr Ala Trp Cys Arg His	
20 25 30	
tgc gac gac gtc att gac gat caa aca ctg ggc ttt cat gcc gac cag	144
Cys Asp Asp Val Ile Asp Asp Gln Thr Leu Gly Phe His Ala Asp Gln	
35 40 45	
ccc tct tcg cag atg cct gag cag cgc ctg cag cag ctt gaa atg aaa	192
Pro Ser Ser Gln Met Pro Glu Gln Arg Leu Gln Gln Leu Glu Met Lys	
50 55 60	
acg cgt cag gcc tac gcc ggt tcg caa atg cac gag ccc gct ttt gcc	240
Thr Arg Gln Ala Tyr Ala Gly Ser Gln Met His Glu Pro Ala Phe Ala	
65 70 75 80	
gcg ttt cag gag gtc gcg atg gcg cat gat atc gct ccc gcc tac gcg	288
Ala Phe Gln Glu Val Ala Met Ala His Asp Ile Ala Pro Ala Tyr Ala	
85 90 95	
ttc gac cat ctg gaa ggt ttt gcc atg gat gtg cgc gaa acg cgc tac	336
Phe Asp His Leu Glu Gly Phe Ala Met Asp Val Arg Glu Thr Arg Tyr	

100					105					110						
ctg	aca	ctg	gac	gat	acg	ctg	cgt	tat	tgc	tat	cac	gtc	gcc	ggt	gtt	384
Leu	Thr	Leu	Asp	Asp	Thr	Leu	Arg	Tyr	Cys	Tyr	His	Val	Ala	Gly	Val	
		115					120					125				
gtg	ggc	ctg	atg	atg	gcg	caa	att	atg	ggc	gtt	cgc	gat	aac	gcc	acg	432
Val	Gly	Leu	Met	Met	Ala	Gln	Ile	Met	Gly	Val	Arg	Asp	Asn	Ala	Thr	
	130					135					140					
ctc	gat	cgc	gcc	tgc	gat	ctc	ggg	ctg	gct	ttc	cag	ttg	acc	aac	att	480
Leu	Asp	Arg	Ala	Cys	Asp	Leu	Gly	Leu	Ala	Phe	Gln	Leu	Thr	Asn	Ile	
	145				150					155					160	
gcg	cgt	gat	att	gtc	gac	gat	gct	cag	gtg	ggc	cgc	tgt	tat	ctg	cct	528
Ala	Arg	Asp	Ile	Val	Asp	Asp	Ala	Gln	Val	Gly	Arg	Cys	Tyr	Leu	Pro	
				165					170					175		
gaa	agc	tgg	ctg	gaa	gag	gaa	gga	ctg	acg	aaa	gcg	aat	tat	gct	gcg	576
Glu	Ser	Trp	Leu	Glu	Glu	Glu	Gly	Leu	Thr	Lys	Ala	Asn	Tyr	Ala	Ala	
			180					185					190			
cca	gaa	aac	cgg	cag	gcc	tta	agc	cgt	atc	gcc	ggg	cga	ctg	gta	cgg	624
Pro	Glu	Asn	Arg	Gln	Ala	Leu	Ser	Arg	Ile	Ala	Gly	Arg	Leu	Val	Arg	
		195					200				205					
gaa	gcg	gaa	ccc	tat	tac	gta	tca	tca	atg	gcc	ggt	ctg	gca	caa	tta	672
Glu	Ala	Glu	Pro	Tyr	Tyr	Val	Ser	Ser	Met	Ala	Gly	Leu	Ala	Gln	Leu	
	210					215					220					
ccc	tta	cgc	tcg	gcc	tgg	gcc	atc	gcg	aca	gcg	aag	cag	gtg	tac	cgt	720
Pro	Leu	Arg	Ser	Ala	Trp	Ala	Ile	Ala	Thr	Ala	Lys	Gln	Val	Tyr	Arg	
	225				230				235						240	
aaa	att	ggc	gtg	aaa	ggt	gaa	cag	gcc	ggt	aag	cag	gcc	tgg	gat	cat	768
Lys	Ile	Gly	Val	Lys	Val	Glu	Gln	Ala	Gly	Lys	Gln	Ala	Trp	Asp	His	
				245					250					255		
cgc	cag	tcc	acg	tcc	acc	gcc	gaa	aaa	tta	acg	ctt	ttg	ctg	acg	gca	816
Arg	Gln	Ser	Thr	Ser	Thr	Ala	Glu	Lys	Leu	Thr	Leu	Leu	Leu	Thr	Ala	
			260					265					270			
tcc	ggt	cag	gca	ggt	act	tcc	cgg	atg	aag	acg	tat	cca	ccc	cgt	cct	864
Ser	Gly	Gln	Ala	Val	Thr	Ser	Arg	Met	Lys	Thr	Tyr	Pro	Pro	Arg	Pro	
		275					280					285				
gct	cat	ctc	tgg	cag	cgc	ccg	atc	tag								891
Ala	His	Leu	Trp	Gln	Arg	Pro	Ile									
	290					295										

<210> 10
 <211> 296
 <212> PRT
 <213> Pantoea stewartii
 <400> 10

Met	Ala	Val	Gly	Ser	Lys	Ser	Phe	Ala	Thr	Ala	Ser	Thr	Leu	Phe	Asp	
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Ala	Lys	Thr	Arg	Arg	Ser	Val	Leu	Met	Leu	Tyr	Ala	Trp	Cys	Arg	His	
			20					25					30			
Cys	Asp	Asp	Val	Ile	Asp	Asp	Gln	Thr	Leu	Gly	Phe	His	Ala	Asp	Gln	
	35						40					45				

Pro Ser Ser Gln Met Pro Glu Gln Arg Leu Gln Gln Leu Glu Met Lys
 50 55 60
 Thr Arg Gln Ala Tyr Ala Gly Ser Gln Met His Glu Pro Ala Phe Ala
 65 70 75 80
 Ala Phe Gln Glu Val Ala Met Ala His Asp Ile Ala Pro Ala Tyr Ala
 85 90 95
 Phe Asp His Leu Glu Gly Phe Ala Met Asp Val Arg Glu Thr Arg Tyr
 100 105 110
 Leu Thr Leu Asp Asp Thr Leu Arg Tyr Cys Tyr His Val Ala Gly Val
 115 120 125
 Val Gly Leu Met Met Ala Gln Ile Met Gly Val Arg Asp Asn Ala Thr
 130 135 140
 Leu Asp Arg Ala Cys Asp Leu Gly Leu Ala Phe Gln Leu Thr Asn Ile
 145 150 155 160
 Ala Arg Asp Ile Val Asp Asp Ala Gln Val Gly Arg Cys Tyr Leu Pro
 165 170 175
 Glu Ser Trp Leu Glu Glu Glu Gly Leu Thr Lys Ala Asn Tyr Ala Ala
 180 185 190
 Pro Glu Asn Arg Gln Ala Leu Ser Arg Ile Ala Gly Arg Leu Val Arg
 195 200 205
 Glu Ala Glu Pro Tyr Tyr Val Ser Ser Met Ala Gly Leu Ala Gln Leu
 210 215 220
 Pro Leu Arg Ser Ala Trp Ala Ile Ala Thr Ala Lys Gln Val Tyr Arg
 225 230 235 240
 Lys Ile Gly Val Lys Val Glu Gln Ala Gly Lys Gln Ala Trp Asp His
 245 250 255
 Arg Gln Ser Thr Ser Thr Ala Glu Lys Leu Thr Leu Leu Leu Thr Ala
 260 265 270
 Ser Gly Gln Ala Val Thr Ser Arg Met Lys Thr Tyr Pro Pro Arg Pro
 275 280 285
 Ala His Leu Trp Gln Arg Pro Ile
 290 295

<210> 11
 <211> 528
 <212> DNA
 <213> Pantoea stewartii

<220>
 <221> CDS
 <222> (1)..(528)

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 atg gaa gtg gtt gct gca ctg gca cat aaa tac atc atg cac ggc tgg 96
 Met Glu Val Val Ala Ala Leu Ala His Lys Tyr Ile Met His Gly Trp
 20 25 30
 ggt tgg ggc tgg cat ctt tca cat cat gaa ccg cgt aaa ggc gca ttt 144
 Gly Trp Gly Trp His Leu Ser His His Glu Pro Arg Lys Gly Ala Phe
 35 40 45
 gaa gtt aac gat ctc tat gcc gtg gta ttc gcc att gtg tcg att gcc 192
 Glu Val Asn Asp Leu Tyr Ala Val Val Phe Ala Ile Val Ser Ile Ala
 50 55 60
 ctg att tac ttc ggc agt aca gga atc tgg ccg ctc cag tgg att ggt 240
 Leu Ile Tyr Phe Gly Ser Thr Gly Ile Trp Pro Leu Gln Trp Ile Gly
 65 70 75 80
 gca ggc atg acc gct tat ggt tta ctg tat ttt atg gtc cac gac gga 288
 Ala Gly Met Thr Ala Tyr Gly Leu Leu Tyr Phe Met Val His Asp Gly
 85 90 95
 ctg gta cac cag cgc tgg ccg ttc cgc tac ata ccg cgc aaa ggc tac 336
 Leu Val His Gln Arg Trp Pro Phe Arg Tyr Ile Pro Arg Lys Gly Tyr
 100 105 110
 ctg aaa cgg tta tac atg gcc cac cgt atg cat cat gct gta agg gga 384
 Leu Lys Arg Leu Tyr Met Ala His Arg Met His His Ala Val Arg Gly
 115 120 125
 aaa gag ggc tgc gtg tcc ttt ggt ttt ctg tac gcg cca ccg tta tct 432
 Lys Glu Gly Cys Val Ser Phe Gly Phe Leu Tyr Ala Pro Pro Leu Ser
 130 135 140
 aaa ctt cag gcg acg ctg aga gaa agg cat gcg gct aga tcg ggc gct 480
 Lys Leu Gln Ala Thr Leu Arg Glu Arg His Ala Ala Arg Ser Gly Ala
 145 150 155 160
 gcc aga gat gag cag gac ggg gtg gat acg tct tca tcc ggg aag taa 528
 Ala Arg Asp Glu Gln Asp Gly Val Asp Thr Ser Ser Ser Gly Lys
 165 170 175

<210> 12
 <211> 175
 <212> PRT
 <213> Pantoea stewartii

<400> 12
 Met Leu Trp Ile Trp Asn Ala Leu Ile Val Phe Val Thr Val Val Gly
 1 5 10 15
 Met Glu Val Val Ala Ala Leu Ala His Lys Tyr Ile Met His Gly Trp
 20 25 30
 Gly Trp Gly Trp His Leu Ser His His Glu Pro Arg Lys Gly Ala Phe
 35 40 45

Glu Val Asn Asp Leu Tyr Ala Val Val Phe Ala Ile Val Ser Ile Ala
 50 55 60
 Leu Ile Tyr Phe Gly Ser Thr Gly Ile Trp Pro Leu Gln Trp Ile Gly
 65 70 75 80
 Ala Gly Met Thr Ala Tyr Gly Leu Leu Tyr Phe Met Val His Asp Gly
 85 90 95
 Leu Val His Gln Arg Trp Pro Phe Arg Tyr Ile Pro Arg Lys Gly Tyr
 100 105 110
 Leu Lys Arg Leu Tyr Met Ala His Arg Met His His Ala Val Arg Gly
 115 120 125
 Lys Glu Gly Cys Val Ser Phe Gly Phe Leu Tyr Ala Pro Pro Leu Ser
 130 135 140
 Lys Leu Gln Ala Thr Leu Arg Glu Arg His Ala Ala Arg Ser Gly Ala
 145 150 155 160
 Ala Arg Asp Glu Gln Asp Gly Val Asp Thr Ser Ser Ser Gly Lys
 165 170 175

<210> 13
 <211> 1860
 <212> DNA
 <213> Methylomonas 16a

<220>
 <221> CDS
 <222> (1)..(1860)

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1 5 10 15	
gcg gac ata cgc gcg ctg tcc aag gac cag ctc cag caa ctg gct gac	96
Ala Asp Ile Arg Ala Leu Ser Lys Asp Gln Leu Gln Gln Leu Ala Asp	
20 25 30	
gag gtg cgc ggc tat ctg acc cac acg gtc agc att tcc ggc ggc cat	144
Glu Val Arg Gly Tyr Leu Thr His Thr Val Ser Ile Ser Gly Gly His	
35 40 45	
ttt gcg gcc ggc ctc ggc acc gtg gaa ctg acc gtg gcc ttg cat tat	192
Phe Ala Ala Gly Leu Gly Thr Val Glu Leu Thr Val Ala Leu His Tyr	
50 55 60	
gtg ttc aat acc ccc gtc gat cag ttg gtc tgg gac gtg ggc cat cag	240
Val Phe Asn Thr Pro Val Asp Gln Leu Val Trp Asp Val Gly His Gln	
65 70 75 80	
gcc tat ccg cac aag att ctg acc ggt cgc aag gag cgc atg ccg acc	288
Ala Tyr Pro His Lys Ile Leu Thr Gly Arg Lys Glu Arg Met Pro Thr	
85 90 95	

att Ile	cg Arg	acc Thr	ctg Leu 100	ggc Gly	ggg Gly	gtg Val	tca Ser	gcc Ala 105	ttt Phe	ccg Pro	gcg Ala	cgg Arg	gac Asp 110	gag Glu	agc Ser	336
gaa Glu	tac Tyr	gat Asp 115	gcc Ala	ttc Phe	ggc Gly	gtc Val	ggc Gly 120	cat His	tcc Ser	agc Ser	acc Thr	tcg Ser 125	atc Ile	agc Ser	gcg Ala	384
gca Ala	ctg Leu 130	ggc Gly	atg Met	gcc Ala	att Ile	gcg Ala 135	tcg Ser	cag Gln	ctg Leu	cg Arg	ggc Gly 140	gaa Glu	gac Asp	aag Lys	aag Lys	432
atg Met 145	gta Val	gcc Ala	atc Ile	atc Ile	ggc Gly 150	gac Asp	ggt Gly	tcc Ser	atc Ile	acc Thr 155	ggc Gly	ggc Gly	atg Met	gcc Ala	tat Tyr 160	480
gag Glu	gcg Ala	atg Met	aat Asn	cat His 165	gcc Ala	ggc Gly	gat Asp	gtg Val	aat Asn 170	gcc Ala	aac Asn	ctg Leu	ctg Leu	gtg Val 175	atc Ile	528
ttg Leu	aac Asn	gac Asp	aac Asn 180	gat Asp	atg Met	tcg Ser	atc Ile	tcg Ser 185	ccg Pro	ccg Pro	gtc Val	ggg Gly	gcg Ala 190	atg Met	aac Asn	576
aat Asn	tat Tyr	ctg Leu 195	acc Thr	aag Lys	gtg Val	ttg Leu	tcg Ser 200	agc Ser	aag Lys	ttt Phe	tat Tyr	tcg Ser 205	tcg Ser	gtg Val	cgg Arg	624
gaa Glu	gag Glu 210	agc Ser	aag Lys	aaa Lys	gct Ala	ctg Leu 215	gcc Ala	aag Lys	atg Met	ccg Pro	tcg Ser 220	gtg Val	tgg Trp	gaa Glu	ctg Leu	672
gcg Ala 225	cg Arg	aag Lys	acc Thr	gag Glu	gaa Glu 230	cac His	gtg Val	aag Lys	ggc Gly	atg Met 235	atc Ile	gtg Val	ccc Pro	ggt Gly	acc Thr 240	720
ttg Leu	ttc Phe	gag Glu	gaa Glu	ttg Leu 245	ggc Gly	ttc Phe	aat Asn	tat Tyr	ttc Phe 250	ggc Gly	ccg Pro	atc Ile	gac Asp	ggc Gly 255	cat His	768
gat Asp	gtc Val	gag Glu	atg Met 260	ctg Leu	gtg Val	tcg Ser	acc Thr	ctg Leu 265	gaa Glu	aat Asn	ctg Leu	aag Lys	gat Asp 270	ttg Leu	acc Thr	816
ggg Gly	ccg Pro	gta Val 275	ttc Phe	ctg Leu	cat His	gtg Val	gtg Val 280	acc Thr	aag Lys	aag Lys	ggc Gly	aaa Lys 285	ggc Gly	tat Tyr	gcg Ala	864
cca Pro	gcc Ala 290	gag Glu	aaa Lys	gac Asp	ccg Pro	ttg Leu 295	gcc Ala	tac Tyr	cat His	ggc Gly	gtg Val 300	ccg Pro	gct Ala	ttc Phe	gat Asp	912
ccg Pro 305	acc Thr	aag Lys	gat Asp	ttc Phe	ctg Leu 310	ccc Pro	aag Lys	gcg Ala	gcg Ala	ccg Pro 315	tcg Ser	ccg Pro	cat His	ccg Pro	acc Thr 320	960
tat Tyr	acc Thr	gag Glu	gtg Val	ttc Phe 325	ggc Gly	cg Arg	tgg Trp	ctg Leu	tgc Cys 330	gac Asp	atg Met	gcg Ala	gct Ala	caa Gln 335	gac Asp	1008
gag Glu	cg Arg	ttg Leu	ctg Leu 340	ggc Gly	atc Ile	acg Thr	ccg Pro	gcg Ala 345	atg Met	cg Arg	gaa Glu	ggc Gly	tct Ser 350	ggt Gly	ttg Leu	1056
gtg Val	gaa Glu	ttc Phe 355	tca Ser	cag Gln	aaa Lys	ttt Phe	ccg Pro 360	aat Asn	cg Arg	tat Tyr	ttc Phe	gat Asp 365	gtc Val	gcc Ala	atc Ile	1104
gcc	gag	cag	cat	gcg	gtg	acc	ttg	gcc	gcc	ggc	cag	gcc	tgc	cag	ggc	1152

Ala	Glu	Gln	His	Ala	Val	Thr	Leu	Ala	Ala	Gly	Gln	Ala	Cys	Gln	Gly	
370						375					380					
gcc	aag	ccg	gtg	gtg	gcg	att	tat	tcc	acc	ttc	ctg	caa	cgc	ggt	tac	1200
Ala	Lys	Pro	Val	Val	Ala	Ile	Tyr	Ser	Thr	Phe	Leu	Gln	Arg	Gly	Tyr	
385					390					395					400	
gat	cag	ttg	atc	cac	gac	gtg	gcc	ttg	cag	aac	tta	gat	atg	ctc	ttt	1248
Asp	Gln	Leu	Ile	His	Asp	Val	Ala	Leu	Gln	Asn	Leu	Asp	Met	Leu	Phe	
				405					410					415		
gca	ctg	gat	cgt	gcc	ggc	ttg	gtc	ggc	ccg	gat	gga	ccg	acc	cat	gct	1296
Ala	Leu	Asp	Arg	Ala	Gly	Leu	Val	Gly	Pro	Asp	Gly	Pro	Thr	His	Ala	
			420					425					430			
ggc	gcc	ttt	gat	tac	agc	tac	atg	cg	tgt	att	ccg	aac	atg	ctg	atc	1344
Gly	Ala	Phe	Asp	Tyr	Ser	Tyr	Met	Arg	Cys	Ile	Pro	Asn	Met	Leu	Ile	
		435					440					445				
atg	gct	cca	gcc	gac	gag	aac	gag	tgc	agg	cag	atg	ctg	acc	acc	ggc	1392
Met	Ala	Pro	Ala	Asp	Glu	Asn	Glu	Cys	Arg	Gln	Met	Leu	Thr	Thr	Gly	
	450					455					460					
ttc	caa	cac	cat	ggc	ccg	gct	tcg	gtg	cg	tat	ccg	cg	ggc	aaa	ggg	1440
Phe	Gln	His	His	Gly	Pro	Ala	Ser	Val	Arg	Tyr	Pro	Arg	Gly	Lys	Gly	
465					470					475					480	
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Pro	Gly	Ala	Ala	Ile	Asp	Pro	Thr	Leu	Thr	Ala	Leu	Glu	Ile	Gly	Lys	
				485					490					495		
gcc	gaa	gtc	aga	cac	cac	ggc	agc	cg	atc	gcc	att	ctg	gcc	tgg	ggc	1536
Ala	Glu	Val	Arg	His	His	Gly	Ser	Arg	Ile	Ala	Ile	Leu	Ala	Trp	Gly	
			500					505					510			
agc	atg	gtc	acg	cct	gcc	gtc	gaa	gcc	ggc	aag	cag	ctg	ggc	gcg	acg	1584
Ser	Met	Val	Thr	Pro	Ala	Val	Glu	Ala	Gly	Lys	Gln	Leu	Gly	Ala	Thr	
		515					520					525				
gtg	gtg	aac	atg	cgt	ttc	gtc	aag	ccg	ttc	gat	caa	gcc	ttg	gtg	ctg	1632
Val	Val	Asn	Met	Arg	Phe	Val	Lys	Pro	Phe	Asp	Gln	Ala	Leu	Val	Leu	
	530					535					540					
gaa	ttg	gcc	agg	acg	cac	gat	gtg	ttc	gtc	acc	gtc	gag	gaa	aac	gtc	1680
Glu	Leu	Ala	Arg	Thr	His	Asp	Val	Phe	Val	Thr	Val	Glu	Glu	Asn	Val	
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atc	gcc	ggc	ggc	gct	ggc	agt	gcg	atc	aac	acc	ttc	ctg	cag	gcg	cag	1728
Ile	Ala	Gly	Gly	Ala	Gly	Ser	Ala	Ile	Asn	Thr	Phe	Leu	Gln	Ala	Gln	
				565					570					575		
aag	gtg	ctg	atg	ccg	gtc	tgc	aac	atc	ggc	ctg	ccc	gac	cg	ttc	gtc	1776
Lys	Val	Leu	Met	Pro	Val	Cys	Asn	Ile	Gly	Leu	Pro	Asp	Arg	Phe	Val	
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gag	caa	ggt	agt	cg	gag	gaa	ttg	ctc	agc	ctg	gtc	ggc	ctc	gac	agc	1824
Glu	Gln	Gly	Ser	Arg	Glu	Glu	Leu	Leu	Ser	Leu	Val	Gly	Leu	Asp	Ser	
		595					600					605				
aag	ggc	atc	ttc	gcc	acc	atc	gaa	cag	ttt	tgc	gct					1860
Lys	Gly	Ile	Phe	Ala	Thr	Ile	Glu	Gln	Phe	Cys	Ala					
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Glu Val Arg Gly Tyr Leu Thr His Thr Val Ser Ile Ser Gly Gly His
35 40 45
Phe Ala Ala Gly Leu Gly Thr Val Glu Leu Thr Val Ala Leu His Tyr
50 55 60
Val Phe Asn Thr Pro Val Asp Gln Leu Val Trp Asp Val Gly His Gln
65 70 75 80
Ala Tyr Pro His Lys Ile Leu Thr Gly Arg Lys Glu Arg Met Pro Thr
85 90 95
Ile Arg Thr Leu Gly Gly Val Ser Ala Phe Pro Ala Arg Asp Glu Ser
100 105 110
Glu Tyr Asp Ala Phe Gly Val Gly His Ser Ser Thr Ser Ile Ser Ala
115 120 125
Ala Leu Gly Met Ala Ile Ala Ser Gln Leu Arg Gly Glu Asp Lys Lys
130 135 140
Met Val Ala Ile Ile Gly Asp Gly Ser Ile Thr Gly Gly Met Ala Tyr
145 150 155 160
Glu Ala Met Asn His Ala Gly Asp Val Asn Ala Asn Leu Leu Val Ile
165 170 175
Leu Asn Asp Asn Asp Met Ser Ile Ser Pro Pro Val Gly Ala Met Asn
180 185 190
Asn Tyr Leu Thr Lys Val Leu Ser Ser Lys Phe Tyr Ser Ser Val Arg
195 200 205
Glu Glu Ser Lys Lys Ala Leu Ala Lys Met Pro Ser Val Trp Glu Leu
210 215 220
Ala Arg Lys Thr Glu Glu His Val Lys Gly Met Ile Val Pro Gly Thr
225 230 235 240
Leu Phe Glu Glu Leu Gly Phe Asn Tyr Phe Gly Pro Ile Asp Gly His
245 250 255
Asp Val Glu Met Leu Val Ser Thr Leu Glu Asn Leu Lys Asp Leu Thr
260 265 270

Gly Pro Val Phe Leu His Val Val Thr Lys Lys Gly Lys Gly Tyr Ala
 275 280 285
 Pro Ala Glu Lys Asp Pro Leu Ala Tyr His Gly Val Pro Ala Phe Asp
 290 295 300
 Pro Thr Lys Asp Phe Leu Pro Lys Ala Ala Pro Ser Pro His Pro Thr
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 Tyr Thr Glu Val Phe Gly Arg Trp Leu Cys Asp Met Ala Ala Gln Asp
 325 330 335
 Glu Arg Leu Leu Gly Ile Thr Pro Ala Met Arg Glu Gly Ser Gly Leu
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 Val Glu Phe Ser Gln Lys Phe Pro Asn Arg Tyr Phe Asp Val Ala Ile
 355 360 365
 Ala Glu Gln His Ala Val Thr Leu Ala Ala Gly Gln Ala Cys Gln Gly
 370 375 380
 Ala Lys Pro Val Val Ala Ile Tyr Ser Thr Phe Leu Gln Arg Gly Tyr
 385 390 395 400
 Asp Gln Leu Ile His Asp Val Ala Leu Gln Asn Leu Asp Met Leu Phe
 405 410 415
 Ala Leu Asp Arg Ala Gly Leu Val Gly Pro Asp Gly Pro Thr His Ala
 420 425 430
 Gly Ala Phe Asp Tyr Ser Tyr Met Arg Cys Ile Pro Asn Met Leu Ile
 435 440 445
 Met Ala Pro Ala Asp Glu Asn Glu Cys Arg Gln Met Leu Thr Thr Gly
 450 455 460
 Phe Gln His His Gly Pro Ala Ser Val Arg Tyr Pro Arg Gly Lys Gly
 465 470 475 480
 Pro Gly Ala Ala Ile Asp Pro Thr Leu Thr Ala Leu Glu Ile Gly Lys
 485 490 495
 Ala Glu Val Arg His His Gly Ser Arg Ile Ala Ile Leu Ala Trp Gly
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 Ser Met Val Thr Pro Ala Val Glu Ala Gly Lys Gln Leu Gly Ala Thr
 515 520 525
 Val Val Asn Met Arg Phe Val Lys Pro Phe Asp Gln Ala Leu Val Leu
 530 535 540

Glu Leu Ala Arg Thr His Asp Val Phe Val Thr Val Glu Glu Asn Val
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Ile Ala Gly Gly Ala Gly Ser Ala Ile Asn Thr Phe Leu Gln Ala Gln
565 570 575

Lys Val Leu Met Pro Val Cys Asn Ile Gly Leu Pro Asp Arg Phe Val
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Lys Gly Ile Phe Ala Thr Ile Glu Gln Phe Cys Ala
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Phe Cys Ala Gly Val Asp Arg Ala Ile Glu Ile Val Asp Gln Ala Ile 25
15 20

gaa gcc ttt ggt gcg ccg att tat gtg cgg cac gag gtg gtg cat aac 147
Glu Ala Phe Gly Ala Pro Ile Tyr Val Arg His Glu Val Val His Asn 35 40
30

cgc acc gtg gtc gat gga ctg aaa caa aaa ggt gcg gtg ttc atc gag 195
Arg Thr Val Val Asp Gly Leu Lys Gln Lys Gly Ala Val Phe Ile Glu 45 55
45 50

gaa cta agc gat gtg ccg gtg ggt tcc tac ttg att ttc agc gcg cac 243
Glu Leu Ser Asp Val Pro Val Gly Ser Tyr Leu Ile Phe Ser Ala His 60 65 70
60 65

ggc gta tcc aag gag gtg caa cag gaa gcc gag gag cgc cag ttg acg 291
Gly Val Ser Lys Glu Val Gln Gln Glu Ala Glu Glu Arg Gln Leu Thr 80 85 90
75 80

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Val Phe Asp Ala Thr Cys Pro Leu Val Thr Lys Val His Met Gln Val 95 100 105
95 100

gcc aag cat gcc aaa cag ggc cga gaa gtg att ttg atc ggc cac gcc 387
Ala Lys His Ala Lys Gln Gly Arg Glu Val Ile Leu Ile Gly His Ala 110 115 120
110 115

ggt cat ccg gaa gtg gaa ggc acg atg ggc cag tat gaa aaa tgc acc 435
Gly His Pro Glu Val Glu Gly Thr Met Gly Gln Tyr Glu Lys Cys Thr 125 130 135
125 130

gaa ggc ggc ggc att tat ctg gtc gaa act ccg gaa gac gta cgc aat 483
Glu Gly Gly Gly Ile Tyr Leu Val Glu Thr Pro Glu Asp Val Arg Asn 135 140 145
135 140

140	145	150	
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caa aac cgt cag gat gcg gtg cat gat ctg gcc aag att tcc gac ctg Gln Asn Arg Gln Asp Ala Val His Asp Leu Ala Lys Ile Ser Asp Leu 205 210 215			675
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gaa atc gcc gtg caa ctc ggt aaa ccc gct tat ttg atc gat act tac Glu Ile Ala Val Gln Leu Gly Lys Pro Ala Tyr Leu Ile Asp Thr Tyr 235 240 245 250			771
cag gat ttg aag caa gat tgg ctg gag gga att gaa gta gtc ggg gtt Gln Asp Leu Lys Gln Asp Trp Leu Glu Gly Ile Glu Val Val Gly Val 255 260 265			819
acc gcg ggc gct tcg gcg ccg gaa gtg ttg gtg cag gaa gtg atc gat Thr Ala Gly Ala Ser Ala Pro Glu Val Leu Val Gln Glu Val Ile Asp 270 275 280			867
caa ctg aag gca tgg ggc ggc gaa acc act tcg gtc aga gaa aac agc Gln Leu Lys Ala Trp Gly Gly Glu Thr Thr Ser Val Arg Glu Asn Ser 285 290 295			915
ggc atc gag gaa aag gta gtc ttt tcg att ccc aag gag ttg aaa aaa Gly Ile Glu Glu Lys Val Val Phe Ser Ile Pro Lys Glu Leu Lys Lys 300 305 310			963
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<400> 16

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Ile Tyr Val Arg His Glu Val Val His Asn Arg Thr Val Val Asp Gly 35 40 45
Leu Lys Gln Lys Gly Ala Val Phe Ile Glu Glu Leu Ser Asp Val Pro 50 55 60

Val Gly Ser Tyr Leu Ile Phe Ser Ala His Gly Val Ser Lys Glu Val
 65 70 75 80
 Gln Gln Glu Ala Glu Glu Arg Gln Leu Thr Val Phe Asp Ala Thr Cys
 85 90 95
 Pro Leu Val Thr Lys Val His Met Gln Val Ala Lys His Ala Lys Gln
 100 105 110
 Gly Arg Glu Val Ile Leu Ile Gly His Ala Gly His Pro Glu Val Glu
 115 120 125
 Gly Thr Met Gly Gln Tyr Glu Lys Cys Thr Glu Gly Gly Ile Tyr
 130 135 140
 Leu Val Glu Thr Pro Glu Asp Val Arg Asn Leu Lys Val Asn Asn Pro
 145 150 155 160
 Asn Asp Leu Ala Tyr Val Thr Gln Thr Thr Leu Ser Met Thr Asp Thr
 165 170 175
 Lys Val Met Val Asp Ala Leu Arg Glu Gln Phe Pro Ser Ile Lys Glu
 180 185 190
 Gln Lys Lys Asp Asp Ile Cys Tyr Ala Thr Gln Asn Arg Gln Asp Ala
 195 200 205
 Val His Asp Leu Ala Lys Ile Ser Asp Leu Ile Leu Val Val Gly Ser
 210 215 220
 Pro Asn Ser Ser Asn Ser Asn Arg Leu Arg Glu Ile Ala Val Gln Leu
 225 230 235 240
 Gly Lys Pro Ala Tyr Leu Ile Asp Thr Tyr Gln Asp Leu Lys Gln Asp
 245 250 255
 Trp Leu Glu Gly Ile Glu Val Val Gly Val Thr Ala Gly Ala Ser Ala
 260 265 270
 Pro Glu Val Leu Val Gln Glu Val Ile Asp Gln Leu Lys Ala Trp Gly
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              Met Lys Gly Ile Cys Ile Leu Gly Ala Thr Gly Ser Ile
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ggt gtc agc acg ctg gat gtc gtt gcc agg cat ccg gat aaa tat caa      159
Gly Val Ser Thr Leu Asp Val Val Ala Arg His Pro Asp Lys Tyr Gln
              15              20              25

gtc gtt gcg ctg acc gcc aac ggc aat atc gac gca ttg tat gaa caa      207
Val Val Ala Leu Thr Asn Gly Asn Ile Asp Ala Leu Tyr Glu Gln
              30              35              40              45

tgc ctg gcc cac cat ccg gag tat gcg gtg gtg gtc atg gaa agc aag      255
Cys Leu Ala His His Pro Glu Tyr Ala Val Val Val Met Glu Ser Lys
              50              55              60

gta gca gag ttc aaa cag cgc att gcc gct tcg ccg gta gcg gat atc      303
Val Ala Glu Phe Lys Gln Arg Ile Ala Ala Ser Pro Val Ala Asp Ile
              65              70              75

aag gtc ttg tcg ggt agc gag gcc ttg caa cag gtg gcc acg ctg gaa      351
Lys Val Leu Ser Gly Ser Glu Ala Leu Gln Gln Val Ala Thr Leu Glu
              80              85              90

aac gtc gat acg gtg atg gcg gct atc gtc ggc gcg gcc gga ttg ttg      399
Asn Val Asp Thr Val Met Ala Ala Ile Val Gly Ala Ala Gly Leu Leu
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ccg acc ttg gcc gcg gcc aag gcc ggc aaa acc gtg ctg ttg gcc aac      447
Pro Thr Leu Ala Ala Ala Lys Ala Gly Lys Thr Val Leu Leu Ala Asn
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aag gaa gcc ttg gtg atg tcg gga caa atc ttc atg cag gcc gtc agc      495
Lys Glu Ala Leu Val Met Ser Gly Gln Ile Phe Met Gln Ala Val Ser
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gat tcc ggc gct gtg ttg ctg ccg ata gac agc gag cac aac gcc atc      543
Asp Ser Gly Ala Val Leu Leu Pro Ile Asp Ser Glu His Asn Ala Ile
              145              150              155

ttt cag tgc atg ccg gcg ggt tat acg cca ggc cat aca gcc aaa cag      591
Phe Gln Cys Met Pro Ala Gly Tyr Thr Pro Gly His Thr Ala Lys Gln
              160              165              170

gcg cgc gcg att tta ttg acc gct tcc ggt ggc cca ttt cga cgg acg      639
Ala Arg Arg Ile Leu Leu Thr Ala Ser Gly Gly Pro Phe Arg Arg Thr
              175              180              185

ccg ata gaa acg ttg tcc agc gtc acg ccg gat cag gcc gtt gcc cat      687
Pro Ile Glu Thr Leu Ser Ser Val Thr Pro Asp Gln Ala Val Ala His
              190              195              200              205

cct aaa tgg gac atg ggg cgc aag att tcg gtc gat tcc gcc acc atg      735
Pro Lys Trp Asp Met Gly Arg Lys Ile Ser Val Asp Ser Ala Thr Met
              210              215              220

atg aac aaa ggt ctc gaa ctg atc gaa gcc tgc ttg ttg ttc aac atg      783
Met Asn Lys Gly Leu Glu Leu Ile Glu Ala Cys Leu Leu Phe Asn Met
              225              230              235

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gag Glu	ccc Pro	gac Asp 240	cag Gln	att Ile	gaa Glu	gtc Val	gtc Val 245	att Ile	cat His	ccg Pro	cag Gln	agc Ser 250	atc Ile	att Ile	cat His	831
tcg Ser	atg Met 255	gtg Val	gac Asp	tat Tyr	gtc Val	gat Asp 260	ggt Gly	tcg Ser	gtt Val	ttg Leu	gcg Ala 265	cag Gln	atg Met	ggt Gly	aat Asn	879
ccc Pro 270	gac Asp	atg Met	cgc Arg	acg Thr	ccg Pro 275	ata Ile	gcg Ala	cac His	gcg Ala	atg Met 280	gcc Ala	tgg Trp	ccg Pro	gaa Glu	cgc Arg 285	927
ttt Phe	gac Asp	tct Ser	ggt Gly	gtg Val 290	gcg Ala	ccg Pro	ctg Leu	gat Asp	att Ile 295	ttc Phe	gaa Glu	gta Val	ggg Gly	cac His 300	atg Met	975
gat Asp	ttc Phe	gaa Glu	aaa Lys 305	ccc Pro	gac Asp	ttg Leu	aaa Lys	cgg Arg 310	ttt Phe	cct Pro	tgt Cys	ctg Leu	aga Arg 315	ttg Leu	gct Ala	1023
tat Tyr	gaa Glu	gcc Ala 320	atc Ile	aag Lys	tct Ser	ggt Gly	gga Gly 325	att Ile	atg Met	cca Pro	acg Thr	gta Val 330	ttg Leu	aac Asn	gca Ala	1071
gcc Ala 335	aat Asn	gaa Glu	att Ile	gct Ala	gtc Val	gaa Glu 340	gcg Ala	ttt Phe	tta Leu	aat Asn	gaa Glu 345	gaa Glu	gtc Val	aaa Lys	ttc Phe	1119
act Thr 350	gac Asp	atc Ile	gcg Ala	gtc Val	atc Ile 355	atc Ile	gag Glu	cgc Arg	agc Ser	atg Met 360	gcc Ala	cag Gln	ttt Phe	aaa Lys	ccg Pro 365	1167
gac Asp	gat Asp	gcc Ala	ggc Gly	agc Ser 370	ctc Leu	gaa Glu	ttg Leu	gtt Val	ttg Leu 375	cag Gln	gcc Ala	gat Asp	caa Gln	gat Asp 380	gcg Ala	1215
cgc Arg	gag Glu	gtg Val	gct Ala 385	aga Arg	gac Asp	atc Ile	atc Ile	aag Lys 390	acc Thr	ttg Leu	gta Val	gct Ala				1254

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35 40 45

His His Pro Glu Tyr Ala Val Val Val Met Glu Ser Lys Val Ala Glu
50 55 60

Phe Lys Gln Arg Ile Ala Ala Ser Pro Val Ala Asp Ile Lys Val Leu
65 70 75 80

Ser Gly Ser Glu Ala Leu Gln Gln Val Ala Thr Leu Glu Asn Val Asp
Page 26

85

90

95

Thr Val Met Ala Ala Ile Val Gly Ala Ala Gly Leu Leu Pro Thr Leu
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 Ala Ala Ala Lys Ala Gly Lys Thr Val Leu Leu Ala Asn Lys Glu Ala
 115 120 125
 Leu Val Met Ser Gly Gln Ile Phe Met Gln Ala Val Ser Asp Ser Gly
 130 135 140
 Ala Val Leu Leu Pro Ile Asp Ser Glu His Asn Ala Ile Phe Gln Cys
 145 150 155 160
 Met Pro Ala Gly Tyr Thr Pro Gly His Thr Ala Lys Gln Ala Arg Arg
 165 170 175
 Ile Leu Leu Thr Ala Ser Gly Gly Pro Phe Arg Arg Thr Pro Ile Glu
 180 185 190
 Thr Leu Ser Ser Val Thr Pro Asp Gln Ala Val Ala His Pro Lys Trp
 195 200 205
 Asp Met Gly Arg Lys Ile Ser Val Asp Ser Ala Thr Met Met Asn Lys
 210 215 220
 Gly Leu Glu Leu Ile Glu Ala Cys Leu Leu Phe Asn Met Glu Pro Asp
 225 230 235 240
 Gln Ile Glu Val Val Ile His Pro Gln Ser Ile Ile His Ser Met Val
 245 250 255
 Asp Tyr Val Asp Gly Ser Val Leu Ala Gln Met Gly Asn Pro Asp Met
 260 265 270
 Arg Thr Pro Ile Ala His Ala Met Ala Trp Pro Glu Arg Phe Asp Ser
 275 280 285
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 305 310 315 320
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 325 330 335
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 340 345 350
 Ala Val Ile Ile Glu Arg Ser Met Ala Gln Phe Lys Pro Asp Asp Ala
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<210> 20
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 <212> DNA
 <213> Artificial sequence

<220>
 <223> Primer #2 for amplification of crt gene cluster

<400> 20
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<210> 21
 <211> 61
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Primer 5'kan(dxs)

<400> 21
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<210> 22
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<220>
 <223> Primer 5'kan(idi)

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<210> 23
 <211> 65
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Primer 5'kan(ygbBP)

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tgtag 65

<210> 24
<211> 60
<212> DNA
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<223> Primer 5'kan(ispAdxs)

<400> 24
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<210> 25
<211> 64
<212> DNA
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<220>
<223> Primer 3'kan

<400> 25
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ttcc 64

<210> 26
<211> 50
<212> DNA
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<223> Primer 5'-T5

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<210> 27
<211> 70
<212> DNA
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<220>
<223> Primer 3'-T5(dxs)

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ctctttaatg 70

<210> 28
<211> 68
<212> DNA
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<220>
<223> Primer 3'-T5(idi)

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ctttaatg 68

<210> 29
 <211> 68
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Primer 3'-T5(ygbBP)

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 ctttaatg 68

<210> 30
 <211> 62
 <212> DNA
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<220>
 <223> Primer 3'-T5(ispAdxs)

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<210> 31
 <211> 65
 <212> DNA
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<220>
 <223> Primer 5'-kanT5(ispB)

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<210> 32
 <211> 67
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Primer 3'-kanT5(ispB)

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 <212> DNA
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<220>
 <223> Phage T5 promoter sequence

<400> 33

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 tcacacagaa ttcattaaag aggagaaatt aactca 156

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 <212> DNA
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<220>
 <223> Primer 5'-kanT5(dxs16a)

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<210> 35
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 tgtag 65

<210> 36
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 <223> Primer 5'-kanT5(lytB16a)

<400> 36
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<210> 37
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<220>
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<400> 37
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<210> 38
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<220>
 <223> Primer 3'-kanT5(dxr16a)

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 <223> Primer 5'-(dxs16a)

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 <223> Primer 5'-(dxr16a)

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 <223> Primer 5'-(lytB16a)

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<210> 43
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 <223> Primer 3'-(dxs16a)

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<210> 44
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 <223> Primer 3'-(dxr16a)
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 <223> Primer T-kan
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 <223> Primer B-ispA
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 <223> Primer B-lytB(16a)

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 <223> Primer Y15_R
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<210> 63
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 <223> Sequence yjeR::Tn5 mutant gene (transposon disrupted yjeR)
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